

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/052,589A
Source: 1FW16
Date Processed by STIC: 11/18/04

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/052,589A

DATE: 11/18/2004

TIME: 09:40:53

Input Set : A:\264734200.ST25.txt

Output Set: N:\CRF4\11182004\J052589A.raw

3 <110> APPLICANT: Perez, Dianne M.
 4 Zuscik, Michael J.
 6 <120> TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disorders
 8 <130> FILE REFERENCE: 26473/04200
 10 <140> CURRENT APPLICATION NUMBER: US 10/052,589A
 11 <141> CURRENT FILING DATE: 2002-01-18
 13 <150> PRIOR APPLICATION NUMBER: US 09/568,255
 14 <151> PRIOR FILING DATE: 2000-05-10
 16 <160> NUMBER OF SEQ ID NOS: 3
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2102
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Mesocricetus sp.
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (15)..(1559)
 28 <223> OTHER INFORMATION:

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35	gca cct gcc caa tgg gga gag ttg aaa gat gcc aac ttc act ggc ccc	98
36	Ala Pro Ala Gln Trp Gly Glu Leu Lys Asp Ala Asn Phe Thr Gly Pro	
37	15 20 25	
39	aac cag acc tcg agc aac tcc aca ctg ccc cag ctg gac gtt acc agg	146
40	Asn Gln Thr Ser Ser Asn Ser Thr Leu Pro Gln Leu Asp Val Thr Arg	
41	30 35 40	
43	gcc atc tct gtg ggc ctg gtg ctg ggc gcc ttc atc ctc ttt gcc att	194
44	Ala Ile Ser Val Gly Leu Val Leu Gly Ala Phe Ile Leu Phe Ala Ile	
45	45 50 55 60	
47	gtg ggc aac atc ctg gtc atc ctg tca gtg gcc tgc aat cgg cac ctg	242
48	Val Gly Asn Ile Leu Val Ile Leu Ser Val Ala Cys Asn Arg His Leu	
49	65 70 75	
51	cgg acg ccc acc aac tac ttc att gtc aac ctg gcc att gct gac ctg	290
52	Arg Thr Pro Thr Asn Tyr Phe Ile Val Asn Leu Ala Ile Ala Asp Leu	
53	80 85 90	
55	ctg ttg agt ttc aca gtc ctg ccc ttc tcc gct acc cta gaa gtg ctt	338
56	Leu Leu Ser Phe Thr Val Leu Pro Phe Ser Ala Thr Leu Glu Val Leu	
57	95 100 105	
59	ggc tac tgg gtt ctg ggg cgc atc ttc tgt gac atc tgg gca gcg gtg	386
60	Gly Tyr Trp Val Leu Gly Arg Ile Phe Cys Asp Ile Trp Ala Ala Val	
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64	Asp	Val	Leu	Cys	Cys	Thr	Ala	Ser	Ile	Leu	Ser	Leu	Cys	Ala	Ile	Ser	
65	125					130				135						140	
67	att	gat	cgc	tac	att	ggg	gtg	cgc	tac	tct	ctg	cag	tac	ccc	act	ctg	482
68	Ile	Asp	Arg	Tyr	Ile	Gly	Val	Arg	Tyr	Ser	Leu	Gln	Tyr	Pro	Thr	Leu	
69					145					150						155	
71	gtc	acc	cgc	agg	aag	gcc	atc	ttg	gca	ctc	ctc	agt	gtg	tgg	gtt	ttg	530
72	Val	Thr	Arg	Arg	Lys	Ala	Ile	Leu	Ala	Leu	Leu	Ser	Val	Trp	Val	Leu	
73				160					165						170		
75	tcc	acg	gtc	atc	tcc	atc	ggg	cct	ctc	ctt	gga	tgg	aaa	gaa	cca	gcg	578
76	Ser	Thr	Val	Ile	Ser	Ile	Gly	Pro	Leu	Leu	Gly	Trp	Lys	Glu	Pro	Ala	
77			175				180						185				
79	ccc	aac	gac	gac	aag	gaa	tgc	gga	gtc	acc	gaa	gaa	ccc	ttc	tat	gcc	626
80	Pro	Asn	Asp	Asp	Lys	Glu	Cys	Gly	Val	Thr	Glu	Glu	Pro	Phe	Tyr	Ala	
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83	ctc	ttt	tcc	tcc	ctg	ggc	tcc	ttc	tac	atc	cca	ctc	gcg	gtc	att	ctg	674
84	Leu	Phe	Ser	Ser	Leu	Gly	Ser	Phe	Tyr	Ile	Pro	Leu	Ala	Val	Ile	Leu	
85	205				210					215						220	
87	gtc	atg	tac	tgc	cgg	gtc	tac	atc	gtg	gcc	aag	agg	acc	acc	aag	aac	722
88	Val	Met	Tyr	Cys	Arg	Val	Tyr	Ile	Val	Ala	Lys	Arg	Thr	Thr	Lys	Asn	
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96	Leu	Arg	Ile	His	Ser	Lys	Asn	Phe	His	Glu	Asp	Thr	Leu	Ser	Ser	Thr	
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99	aag	gcc	aag	ggc	cac	aac	ccc	agg	agt	tcc	ata	gct	gtc	aaa	ctt	ttt	866
100	Lys	Ala	Lys	Gly	His	Asn	Pro	Arg	Ser	Ser	Ile	Ala	Val	Lys	Leu	Phe	
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108	Gly	Met	Phe	Ile	Leu	Cys	Trp	Leu	Pro	Phe	Phe	Ile	Ala	Leu	Pro	Leu	
109				305					310						315		
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112	Gly	Ser	Leu	Phe	Ser	Thr	Leu	Lys	Pro	Pro	Asp	Ala	Val	Phe	Lys	Val	
113			320						325					330			
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116	Val	Phe	Trp	Leu	Gly	Tyr	Phe	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Ile	Tyr	
117		335				340							345				
119	ccg	tgc	tcc	agc	aag	gag	ttc	aag	cgc	gcc	ttc	atg	cgt	atc	ctt	ggg	1106
120	Pro	Cys	Ser	Ser	Lys	Glu	Phe	Lys	Arg	Ala	Phe	Met	Arg	Ile	Leu	Gly	
121		350				355						360					
123	tgc	cag	tgc	cgt	agt	ggc	cgt	cgc	cgc	cgc	cgc	cgt	cgt	ctg	ggc		1154
124	Cys	Gln	Cys	Arg	Ser	Gly	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Leu	Gly	
125	365				370				375						380		
127	gcg	tgc	gct	tac	acc	tat	cgg	ccg	tgg	acg	cgc	ggc	ggc	tcg	ctg	gag	1202

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132 Arg Ser Gln Ser Arg Lys Asp Ser Leu Asp Asp Ser Gly Ser Cys Met
133           400           405           410
135 agt ggc agc cag agg acc ctg ccc tcg gcg tcg ccc agc ccg ggc tac      1298
136 Ser Gly Ser Gln Arg Thr Leu Pro Ser Ala Ser Pro Ser Pro Gly Tyr
137           415           420           425
139 ctg ggt cgc gga gcg cag cca cca ctg gag ctg tgc gcc tac ccc gaa      1346
140 Leu Gly Arg Gly Ala Gln Pro Leu Glu Leu Cys Ala Tyr Pro Glu
141           430           435           440
143 tgg aaa tcc ggg gct ctg ctc agt ctg cca gag cct ccg ggt cgc cgc      1394
144 Trp Lys Ser Gly Ala Leu Leu Ser Leu Pro Glu Pro Pro Gly Arg Arg
145 445           450           455           460
147 ggt cgc ctc gac tct ggg ccc ctc ttc act ttc aag ctc ttg gga gag      1442
148 Gly Arg Leu Asp Ser Gly Pro Leu Phe Thr Phe Lys Leu Leu Gly Glu
149           465           470           475
151 ccg gag agc ccg ggc acc gag ggc gat gcc agc aat ggg ggc tgc gac      1490
152 Pro Glu Ser Pro Gly Thr Glu Gly Asp Ala Ser Asn Gly Gly Cys Asp
153           480           485           490
155 gca acg acc gac ctg gcc aat ggg cag ccc ggt ttc aag agc aac atg      1538
156 Ala Thr Thr Asp Leu Ala Asn Gly Gln Pro Gly Phe Lys Ser Asn Met
157           495           500           505
159 cct ctg gca ccc ggg cac ttt taggggtccct tttctttccc ccacacacac      1589
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161           510           515
163 cccagggggg aggacacccat tgtggggggg ggggggcatgg gggggagtggt cagccccggg      1649
165 tagacacagg gtcgcaaggg tacaagggggg gagggggggcg gggagagggg cagctgcttt      1709
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171 tataaagagt ccctctatac gtatttatct gtgggtacac gtgcgtgtgt ctgtgcggtg      1889
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198           35           40           45
201 Gly Leu Val Leu Gly Ala Phe Ile Leu Phe Ala Ile Val Gly Asn Ile
202           50           55           60
205 Leu Val Ile Leu Ser Val Ala Cys Asn Arg His Leu Arg Thr Pro Thr

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214          100          105          110
217 Leu Gly Arg Ile Phe Cys Asp Ile Trp Ala Ala Val Asp Val Leu Cys
218          115          120          125
221 Cys Thr Ala Ser Ile Leu Ser Leu Cys Ala Ile Ser Ile Asp Arg Tyr
222          130          135          140
225 Ile Gly Val Arg Tyr Ser Leu Gln Tyr Pro Thr Leu Val Thr Arg Arg
226 145          150          155          160
229 Lys Ala Ile Leu Ala Leu Leu Ser Val Trp Val Leu Ser Thr Val Ile
230          165          170          175
233 Ser Ile Gly Pro Leu Leu Gly Trp Lys Glu Pro Ala Pro Asn Asp Asp
234          180          185          190
237 Lys Glu Cys Gly Val Thr Glu Glu Pro Phe Tyr Ala Leu Phe Ser Ser
238          195          200          205
241 Leu Gly Ser Phe Tyr Ile Pro Leu Ala Val Ile Leu Val Met Tyr Cys
242          210          215          220
245 Arg Val Tyr Ile Val Ala Lys Arg Thr Thr Lys Asn Leu Glu Ala Gly
246 225          230          235          240
249 Val Met Lys Glu Met Ser Asn Ser Lys Glu Leu Thr Leu Arg Ile His
250          245          250          255
253 Ser Lys Asn Phe His Glu Asp Thr Leu Ser Ser Thr Lys Ala Lys Gly
254          260          265          270
257 His Asn Pro Arg Ser Ser Ile Ala Val Lys Leu Phe Lys Phe Ser Arg
258          275          280          285
261 Glu Lys Lys Ala Ala Lys Thr Leu Gly Ile Val Val Gly Met Phe Ile
262          290          295          300
265 Leu Cys Trp Leu Pro Phe Phe Ile Ala Leu Pro Leu Gly Ser Leu Phe
266 305          310          315          320
269 Ser Thr Leu Lys Pro Pro Asp Ala Val Phe Lys Val Val Phe Trp Leu
270          325          330          335
273 Gly Tyr Phe Asn Ser Cys Leu Asn Pro Ile Ile Tyr Pro Cys Ser Ser
274          340          345          350
277 Lys Glu Phe Lys Arg Ala Phe Met Arg Ile Leu Gly Cys Gln Cys Arg
278          355          360          365
281 Ser Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Leu Gly Ala Cys Ala Tyr
282          370          375          380
285 Thr Tyr Arg Pro Trp Thr Arg Gly Gly Ser Leu Glu Arg Ser Gln Ser
286 385          390          395          400
289 Arg Lys Asp Ser Leu Asp Asp Ser Gly Ser Cys Met Ser Gly Ser Gln
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293 Arg Thr Leu Pro Ser Ala Ser Pro Ser Pro Gly Tyr Leu Gly Arg Gly
294          420          425          430
297 Ala Gln Pro Pro Leu Glu Leu Cys Ala Tyr Pro Glu Trp Lys Ser Gly
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305 Ser Gly Pro Leu Phe Thr Phe Lys Leu Leu Gly Glu Pro Glu Ser Pro
306 465                               470                               475                               480
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331 tctctaaagg cagcttaggt aagatagttg aaatgagggc agggactgtt ttcaaagcta      180
333 tctgaatcat tgtttgtttg tttgtttgtt tgttatctca gagaaactcc ttagaattgt      240
335 atattttgtg caactggaga gcttgtgcca tttttaatag gagattaagg accttaaagc      300
337 tatagtgggt gatacatgct tgtaacaaca acactaagag gctgggaaaa gaggaagatt      360
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341 aagaccatct ctcaacaag caatcaaagg ctggagagtt gtctcagcag ataagggcat      480
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